

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 30, 2005, 12:01:52 ; Search time 39 Seconds

(without alignments)  
244.243 Million cell updates/sec

Title: US-09-941-997-2

Perfect score: 495

Sequence: 1 MADGSSDAAREPRAPAPAPR.....COPELAGLGFAPQLDLCRQ 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	100.0	210	1 TPRBUC	troponin I, cardia
2	441.5	89.2	211	1 TPRBUC	troponin I, cardia
3	440.5	89.0	211	2 A53805	troponin I, cardia
4	438.5	88.6	211	2 A60124	troponin I, cardia
5	435.5	88.0	211	2 I56441	troponin I - rat
6	413	83.4	211	2 A29994	troponin I, cardia
7	301.5	60.9	208	2 A41030	cardiac troponin I
8	294.5	59.5	244	2 I51408	troponin I, cardia
9	164	33.1	187	2 B44786	troponin I, slow s
10	154	31.1	187	1 TPRBUC	troponin I, slow s
11	142	28.7	184	1 TPRBUC	troponin I, slow s
12	129.5	26.2	182	1 TPRBIS	troponin I, fast s
13	129.5	26.2	182	2 A47816	troponin I, fast s
14	126.5	25.6	182	1 TPRBIS	troponin I, fast s
15	122.5	24.7	142	2 JC5612	troponin I beta -
16	121.5	24.5	142	2 JC5611	troponin I alpha -
17	120.5	24.3	208	2 A40547	troponin I - fruit
18	119.5	24.1	183	1 TPRBIS	troponin I, fast s
19	119.5	24.1	183	2 A23569	troponin I, fast s
20	118.5	23.9	173	2 JC5610	troponin I - sea s
21	113.5	22.9	260	2 B38594	troponin I - fruit
22	109.5	22.1	201	2 A14844	troponin I, fast s
23	103.5	20.9	208	2 A38594	troponin I - fruit
24	96.5	19.5	176	2 S70008	troponin I - Atlan
25	86.5	17.5	260	2 T25017	hypothetical prote
26	82.5	16.7	292	2 JE0233	troponin-I - scall
27	74.5	15.1	742	2 T38001	probable phosphati
28	74	14.9	233	2 T17218	hypothetical prote
29	73.5	14.8	327	2 S49619	crta protein - Rho

30	72.5	14.6	335	2 T33457	hypothetical prote
31	72.5	14.6	338	2 I53043	transforming prote
32	72	14.5	886	2 S07132	hypothetical prote
33	72	14.5	1415	1 EDBEGA	immediate-early pr
34	71.5	14.4	306	2 T27985	hypothetical prote
35	71.5	14.4	324	2 F64592	hypothetical prote
36	71.5	14.4	351	2 B34768	ORF5 protein - Orf
37	71	14.3	197	2 T15106	hypothetical prote
38	70.5	14.2	314	2 JC4951	troponin T - scall
39	70.5	14.2	327	2 T50744	spheroidene monoox
40	70.5	14.2	387	2 S02708	troponin T - fruit
41	70.5	14.2	462	2 T46215	hypothetical prote
42	70	14.1	303	2 A48130	growth arrest-spec
43	70	14.1	2957	2 T33152	hypothetical prote
44	69.5	14.0	263	2 A34466	calpain EC 3.4.22
45	69.5	14.0	344	2 F98307	hypothetical prote

## ALIGNMENTS

## RESULT 1

## TPBUC

troponin I, cardiac muscle - human

C:Species: Homo sapiens (man)

C:Date: 03-May-1994 #sequence revision 03-May-1996 #text\_change 09-Jul-2004

C:Accession: A61229; JN0837; S11522; A33185; S63690

R:Hunkeler, N.M.; Kullman, J.; Murphy, A.M.

C:Gene: 151287, 151288, 151289, 151290, 151291, 151292, 151293, 151294, 151295, 151296, 151297, 151298, 151299, 151300, 151301, 151302, 151303, 151304, 151305, 151306, 151307, 151308, 151309, 151310, 151311, 151312, 151313, 151314, 151315, 151316, 151317, 151318, 151319, 151320, 151321, 151322, 151323, 151324, 151325, 151326, 151327, 151328, 151329, 151330, 151331, 151332, 151333, 151334, 151335, 151336, 151337, 151338, 151339, 151340, 151341, 151342, 151343, 151344, 151345, 151346, 151347, 151348, 151349, 151350, 151351, 151352, 151353, 151354, 151355, 151356, 151357, 151358, 151359, 151360, 151361, 151362, 151363, 151364, 151365, 151366, 151367, 151368, 151369, 151370, 151371, 151372, 151373, 151374, 151375, 151376, 151377, 151378, 151379, 151380, 151381, 151382, 151383, 151384, 151385, 151386, 151387, 151388, 151389, 151390, 151391, 151392, 151393, 151394, 151395, 151396, 151397, 151398, 151399, 151400, 151401, 151402, 151403, 151404, 151405, 151406, 151407, 151408, 151409, 151410, 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```
RESULT 5
156441
troponin I - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I56441
J/Martin, A.F.; Orłowski, J.
J. Mol. Cell. Cardiol. 23, 583-588, 1991
A/Title: Molecular cloning and developmental expression of the rat cardiac-specific isoform of troponin I
A/Reference number: I56441; MUID:91359315; PMID:1886137
A/Accession: I56441
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-211 <RES>
A/Cross-references: UNIPROT:P23693; GB:M92074; NID:g207515; PIDN:AAA42294.1; PID:g207516
C/Superfamily: troponin I

Query Match      88.0%; Score 435.5; DB 2; Length 211;
Best Local Similarity 88.0%; Pred. No. 1.2e-33;
Matches 88; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

Qy 1 MADSSDAARPRPAPAPIRRRSS-NYRAYATEPHAKKSKISASRKLQKTLTLLQIAKQ 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MADSSDAGAPAPAPRRRRSSNYRAYATEPHAKKSKISASRKLQKTLTLLQIAKQ 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 ELERAEEREGKGRALSTRCQPLEAGLGFPAELQDLCRQ 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 EMERAEEREGKGRVLTSTRCQPLVDGLGFEEQLQDLCRQ 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
A29994
troponin I, cardiac muscle - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29994; S02628
R/Leazyk, J.; Dumaswala, R.; Potter, J.D.; Collins, J.H.
Biochemistry 27, 2821-2827, 1988
A/Title: Amino acid sequence of bovine cardiac troponin I.
A/Reference number: A29994; MUID:88294022; PMID:3042023
A/Accession: A29994
A/Molecule type: protein
A/Residues: 1-211 <RES>
A/Cross-references: UNIPROT:P08057
R/Swidersek, K.; Jaquet, K.; Meyer, H.E.; Heilmeyer Jr., L.M.G.
Eur. J. Biochem. 176, 335-342, 1988
A/Title: Cardiac troponin I, isolated from bovine heart, contains two adjacent phosphoserine residues
A/Reference number: S02628; MUID:88329087; PMID:3138117
A/Accession: S02628
A/Molecule type: protein
A/Residues: 21-27,'Y',28-37 <SWT>
A/Note: authors comment in a note added in proof that the extra tyrosine is an error
C/Superfamily: troponin I
C/Keywords: acetylated amino end; actin binding; cardiac muscle; heart; muscle; phosphoprotein; phosphorylated; phosphorylation; phosphorylated amino end (Ala) #status experimental
F/23,24/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match      83.4%; Score 413; DB 2; Length 211;
Best Local Similarity 87.0%; Pred. No. 1.6e-31;
Matches 87; Conservative 3; Mismatches 8; Indels 2; Gaps 2;

Qy 2 ADGSSDAARPRPAPAPIRRRSS-NYRAYATEPHAKKSKISASRKLQKTLTLLQIAKQ 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ADRSGGSGTAGTVAPPPVRRSSNYRAYATEPHAKKSKISASRKLQKTLTLLQIAKQ 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 ELERAEEREGKGRALSTRCQPLEAGLGFPAELQDLCRQ 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ELERAEEREGKGRALSTRCQPLEAGLGFPAELQDLCRQ 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
A41030
troponin I, cardiac muscle - quail
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C/Species: Coturnix coturnix (quail)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Aug-1999
C/Accession: A41030
R/Hastings, K.E.M.; Koppe, R.I.; Marmor, E.; Bader, D.; Shimada, Y.; Toyota, N.
J. Biol. Chem. 266, 19659-19665, 1991
A/Title: Structure and developmental expression of troponin I isoforms. cDNA clone anal
A/Reference number: A41030; MUID:92011768; PMID:1918073
A/Accession: A41030
A/Molecule type: mRNA
A/Residues: 1-208 <HAS>
A/Cross-references: GB:M73702; NID:g213647; PIDN:AAA49513.1; PID:g213648
C/Superfamily: troponin I
C/Keywords: actin binding; cardiac muscle; heart

Query Match      60.9%; Score 301.5; DB 2; Length 208;
Best Local Similarity 67.4%; Pred. No. 4.1e-21;
Matches 62; Conservative 10; Mismatches 19; Indels 1; Gaps 1;

Qy 9 ARPRPAPAPIRRRSS-NYRAYATEPHAKKSKISASRKLQKTLTLLQIAKQELERAE 67
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 AESEEPKPPPLRRKSSANYRGYAVEPHAKRQSKISASRKLQKTLTLLQRAKRDLEBEQE 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 68 RREKGRALSTRCQPLEAGLGFPAELQDLCRQ 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 RAGEKORHGLGELCPPPELDGLGVAQLQELCRE 93
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
I51408
cardiac troponin I - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I51408
R/Drysdale, T.A.; Tonissen, K.F.; Patterson, K.D.; Crawford, M.J.; Krieg, P.A.
Dev. Biol. 165, 432-441, 1994
A/Title: Cardiac troponin I is a heart-specific marker in the Xenopus embryo: expressio
A/Reference number: I51408; MUID:95046865; PMID:7958411
A/Accession: I51408
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-244 <DRY>
A/Cross-references: UNIPROT:P50754; GB:L25721; NID:g410050; PIDN:AAA65727.1; PID:g41005
C/Superfamily: troponin I
C/Keywords: cardiac muscle; heart

Query Match      59.5%; Score 294.5; DB 2; Length 244;
Best Local Similarity 62.8%; Pred. No. 2.2e-20;
Matches 62; Conservative 12; Mismatches 18; Indels 7; Gaps 2;

Qy 8 AAREPRPAPAP-----IRRRSS-NYRAYATEPHAKKSKISASRKLQKTLTLLQIAKQE 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 26 ADEPPKAPPPAPPPPLIRRRSSANYRSVATEPQVKKPKISASRKLQNTMTMLQIAKAE 85
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 LEREAEEREGKGRALSTRCQPLEAGLGFPAELQDLCRQ 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 86 MEREEERARERKERYLAHCQPLQLSGLSRSELQDLQCE 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
B44786
troponin I, slow skeletal muscle - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C/Accession: B44786
R/Koppe, R.I.; Hallauer, P.L.; Karpatis, G.; Hastings, K.E.M.
J. Biol. Chem. 264, 14327-14333, 1989
A/Title: cDNA clone and expression analysis of rodent fast and slow skeletal muscle tro
A/Reference number: A44786; MUID:89340548; PMID:2760067
A/Accession: B44786
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-187 <KOP>
A/Cross-references: UNIPROT:PI3413; GB:J04993; NID:g207517; PIDN:AAA442295.1; PID:g20751
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Nature 211, 31-35, 1978  
 A>Title: Comparison of amino acid sequence of troponin I from different striated muscles  
 A'Reference number: A93193; MUID:78114026; PMID:146828  
 A'Accession: A93193  
 A'Molecule type: protein  
 A'Residuals: 2-154,158-182 <WIL>  
 R:Wilkinson, J.M.; Grand, R.J.A.  
 Biochem. J. 149, 493-496, 1975  
 A>Title: The amino acid sequence of troponin I from rabbit skeletal muscle.  
 A'Reference number: A90286; MUID:76039510; PMID:1180911  
 A'Accession: A90286  
 A'Molecule type: protein  
 A'Residuals: 2-114, 'R4, 115-154, 158-182 <W12>  
 R:Moir, A.J.G.; Wilkinson, J.M.; Perry, S.V.  
 FEBS Lett. 42, 253-256, 1974  
 A>Title: The phosphorylation sites of troponin I from white skeletal muscle of the rabbit  
 A'Reference number: A31408; MUID:74309023; PMID:4369337  
 A'Contents: annotation; phosphorylation sites  
 R:Huang, T.S.; Bylund, D.B.; Stull, J.T.; Krebs, E.G.  
 FEBS Lett. 42, 249-252, 1974  
 A>Title: The amino acid sequences of the phosphorylated sites in troponin-I from rabbit  
 A'Reference number: A31407; MUID:74308154; PMID:4369265  
 A'Contents: annotation; phosphorylation sites  
 R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.  
 Nature 302, 718-721, 1983  
 A>Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by shot

A;Reference number: I46471; MUID:83167564; PMID:6687628  
A;Accession: I46514

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 166-178 <PUT>

A;Cross-references: EMBL:V00898; NID:gl738; PIDN:CAA24263.1; PID:g929767

C;Complex: troponin is a heterotrimer with one molecule each of troponin C (calcium binding)

C;Function: binds actin and inhibits myosin ATPase activity; with tropomyosin mediated

A;Pathway: muscle contraction

C;Superfamily: troponin I

C;Keywords: acetylated amino end; actin binding; muscle contraction; phosphoprotein; skeletal

F;2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental

F;12/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status experim

F;20,90,118/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status

Query Match 26.2%; Score 129.5; DB 1; Length 182;

Best Local Similarity 42.2%; Pred. No. 4.5e-05;

Matches 27; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

36 KKSKISASRKQLKTLQLIAKQELERAEERGERGKRALSTRCQPLELAGLGFALQD 95

5 EKNRAITARRQHLKSVMLQIAATELEKEERREAEKQNYLAHCPLSLPG-SMASEVQE 63

96 LCRQ 99

64 LCKQ 67

#### RESULT 13

A44786

troponin I, fast skeletal muscle - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1993 #sequence\_revision 19-Mar-1993 #text\_change 09-Jul-2004

C;Accession: A44786

R;Koppe, R.I.; Hallauer, P.L.; Karpatti, G.; Hastings, K.E.M.

J. Biol. Chem. 264, 14327-14333, 1989

A;Title: cDNA clone and expression analysis of rodent fast and slow skeletal muscle trop

A;Reference number: A44786; MUID:89340548; PMID:2760067

A;Accession: A44786

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-182 <KOP>

A;Cross-references: UNIPROT:P13412; GB:J04992; NID:G202164; PIDN:AAA40485.1; PID:G202165

C;Superfamily: troponin I

C;Keywords: skeletal muscle

Query Match 26.2%; Score 129.5; DB 2; Length 182;

Best Local Similarity 40.6%; Pred. No. 4.5e-05;

Matches 26; Conservative 15; Mismatches 22; Indels 1; Gaps 1;

36 KKSKISASRKQLKTLQLIAKQELERAEERGERGKRALSTRCQPLELAGLGFALQD 95

5 EKNRAITARRQHLKSVMLQIAATELEKEERREAEKQNYLAHCPLSLPG-SMASEVQE 63

96 LCRQ 99

64 LCKQ 67

#### RESULT 14

TPHUIS

troponin I, fast skeletal muscle - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004

C;Accession: S43508

R;Zhu, L.; Perez-Alvarado, G.; Wade, R.

Biochim. Biophys. Acta 1217, 338-340, 1994

A;Title: Sequencing of a cDNA encoding the human fast-twitch skeletal muscle isoform of

A;Reference number: S43508; MUID:94198300; PMID:8148383

A;Accession: S43508

A;Molecule type: mRNA

A;Residues: 1-182 <ZHU>

A;Cross-references: UNIPROT:P48788; GB:L21715; NID:G452077; PIDN:AAA19813.1; PID:G45207;

C;Genetics:

A;Gene: GDB:TNNI2

A;Cross-references: GDB:125308; OMIM:191043

A;Map position: 1q32-1q32

C;Complex: troponin is a heterotrimer with one molecule each of troponin C (calcium binding)

C;Function: binds actin and inhibits myosin ATPase activity; with tropomyosin mediated

A;Pathway: muscle contraction

C;Superfamily: troponin I

C;Keywords: acetylated amino end; actin binding; muscle contraction; skeletal muscle

F;2/Modified site: acetylated amino end (Gly) (in mature form) #status predicted

Query Match 25.6%; Score 126.5; DB 1; Length 182;

Best Local Similarity 39.1%; Pred. No. 8.6e-05;

Matches 25; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

36 KKSKISASRKQLKTLQLIAKQELERAEERGERGKRALSTRCQPLELAGLGFALQD 95

5 EKNRAITARRQHLKSVMLQIAATELEKEERREAEKQNYLAHCPLSLPG-SMASEVQE 63

96 LCRQ 99

64 LCKQ 67

#### RESULT 15

JC5612

troponin I beta - sea squirt (Halocynthia roretzi)

C;Species: Halocynthia roretzi

C;Date: 23-Sep-1997 #sequence\_revision 17-Oct-1997 #text\_change 09-Jul-2004

C;Accession: JC5612

R;Yuasa, H.J.; Sato, S.; Yamamoto, H.; Takagi, T.

J. Biochem. 122, 374-380, 1997

A;Title: Primary structure of troponin I isoforms from the ascidian Halocynthia roretzi

A;Reference number: JC5610; MUID:98021076; PMID:9378716

A;Accession: JC5612

A;Molecule type: mRNA

A;Residues: 1-142 <YUA>

A;Cross-references: UNIPROT:O01356; DBJ:AB001687; NID:gi888348; PIDN:BAAL9427.1; PID:gi

A;Experimental source: Halocynthia roretzi larva

C;Comment: This protein binds to actin, and inhibits the interaction between actin and

C;Superfamily: troponin I

Query Match 24.7%; Score 122.5; DB 2; Length 142;

Best Local Similarity 48.2%; Pred. No. 0.00016;

Matches 27; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

45 RKQLKTLQLIAKQELERAEERGERGKRALSTRCQPL-ELAGLGFALQDLCRQ 99

5 RKQLKSLLSRAREDLKREBEQKAEKKILSNRIESLGLDLSMSQQLMELCRE 60

96 LCRQ 99

64 LCKQ 67

Search completed: August 30, 2005, 12:12:25

Job time : 41 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 11:53:31 ; Search time 168 Seconds  
(without alignments)  
301.761 Million cell updates/sec

Title: US-09-941-997-2

Perfect score: 495

Sequence: 1 MADGSSDAAREPRPAPAPIR.....COPLAAGLPABQLDLCRQ 99

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	491	99.2	210	Q6FGU5	Q6fgu5 homo sapien
2	490	99.0	209	1 TRIC_HUMAN	P19429 homo sapien
3	443.5	89.6	211	Q8MKD5	Q8mkd5 canis famil
4	439.5	88.8	211	1 TRIC_RABIT	P02645 oryctolagus
5	435.5	88.0	210	1 TRIC_MOUSE	P48787 mus musculus
6	435	87.9	210	2 Q863B6	Q863b6 felis silve
7	433.5	87.6	210	1 TRIC_RAT	P23693 rattus norv
8	413	83.4	211	1 TRIC_BOVIN	P08057 bos taurus
9	305.5	61.7	208	2 Q6S7R4	Q6s7r4 melesgris g
10	305.5	61.7	208	2 Q6S7R5	Q6s7r5 melesgris g
11	305.5	61.7	208	2 Q6S7R6	Q6s7r6 gallus gall
12	301.5	60.9	207	1 TRIC_COTUA	P27672 coturnix co
13	296.5	59.9	246	2 Q63ZJ0	Q63zj0 xenopus lae
14	294.5	59.5	243	1 TRIC_XENLA	P50754 xenopus lae
15	293.5	59.3	238	2 Q6YA69	Q6ya69 rana catesb
16	175	35.4	168	1 TRIC_CHICK	P27673 gallus gall
17	166	33.5	198	2 Q6DHL8	Q6dhl8 brachydanio
18	164	33.1	186	1 TRIS_MOUSE	Q9wuz5 mus musculus
19	164	33.1	186	1 TRIS_RAT	P13413 rattus norv
20	163.5	33.0	188	2 Q90350	Q90350 coturnix co
21	154	31.1	186	1 TRIS_HUMAN	P19237 homo sapien
22	154	31.1	187	2 Q96DT9	Q96dt9 homo sapien
23	154	31.1	187	2 Q6FGH1	Q6fgw1 homo sapien
24	154	31.1	187	2 Q6ICU2	Q6icu2 homo sapien
25	154	31.1	187	2 Q96T57	Q96t57 homo sapien
26	154	31.1	187	2 Q7YSF4	Q7ysf4 sus scrofa
27	151	30.5	108	2 Q95KL2	Q95kl2 capra hircu
28	151	30.5	183	2 Q8QGC5	Q8qgc5 xenopus lae
29	151	30.5	183	2 Q7SYI1	Q7syi1 xenopus lae
30	149	30.1	183	2 Q6P8F9	Q6p8f9 xenopus tro
31	147	29.7	260	2 Q8WPC1	Q8wpc1 halocynthia

32 144 29.1 183 2 Q6GNQ7 Q6gnq7 xenopus lae  
33 143 28.9 181 2 Q8AW33 Q8aw33 brachydanio  
34 142 28.7 184 1 TRIS\_RABIT P02645 oryctolagus  
35 135 27.3 187 2 Q6YA68 Q6ya68 rana catesb  
36 133 26.9 180 2 Q6IQ92 Q6iq92 brachydanio  
37 130.5 26.4 149 2 Q01356 Q01356 halocynthia  
38 130.5 26.4 182 2 Q8QGC6 Q8qgc6 xenopus lae  
39 129.5 26.2 181 1 TRIF\_MOUSE P13412 mus musculus  
40 129.5 26.2 181 1 TRIF\_RABIT P02643 oryctolagus  
41 129.5 26.2 181 1 TRIF\_RAT P27768 rattus norv  
42 127.5 25.8 149 2 Q8WSF5 Q8wsp5 halocynthia  
43 126.5 25.6 149 2 Q01355 Q01355 halocynthia  
44 126.5 25.6 181 1 TRIF\_HUMAN P48788 homo sapien  
45 126.5 25.6 199 2 Q6IMC7 Q6imc7 drosophila

#### ALIGNMENTS

RESULT 1  
Q6FGU5 PRELIMINARY; PRT; 210 AA.  
AC Q6FGU5, AC Q6FGU5, PRT; 210 AA.  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE TNNI3 protein (Fragment).  
GN Name=TNNI3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,  
RA Neubert P., Kstrang K., Schattner R., Shen B., Henze S., Mar W.,  
RA Korn B., Zuo D., Hu Y., LaBaer J.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR542012; CAG46809.1;  
DR GO; GO:0030484; C-muscle fiber; IEA.  
DR InterPro; IPR001978; Troponin.  
DR Pfam; PF00992; Troponin; 1.  
FT NON TER 210 210  
SQ SEQUENCE 210 AA; 24019 MW; ECEA9DEAC24A78BD CRC64;  
Query Match 99.2%; Score 491; DB 2; Length 210;  
Best Local Similarity 99.0%; Pred. No. 3.le-38;  
Matches 99; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKISASRKQLKTLTLLQIAKOE 60  
DB 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKISASRKQLKTLTLLQIAKOE 60  
QY 61 LEREABERGEKGRALSTRCPLELAGLPABQLDLCRQ 99  
DB 61 LEREABERGEKGRVLSRCPLELAGLPABQLDLCRQ 99

RESULT 2  
TRIC\_HUMAN STANDARD; PRT; 209 AA.  
ID TRIC\_HUMAN  
AC P19429;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Troponin I, cardiac muscle.  
GN Name=TNNI3; Synonyms=TNNC1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Heart muscle;  
 RX MEDLINE=9102031; PubMed=2226790; DOI=10.1016/0014-5793(90)81234-F;  
 RA Vallins W.J., Brand N.J., Dabhadre N., Butler-Browne G., Yacoub M.H.,  
 RA Barton P.J.R.;  
 RT "Molecular cloning of human cardiac troponin I using polymerase chain  
 RT reaction.";  
 RL FEBS Lett. 270:57-61(1990).  
 RN [2]  
 RP REVISION TO 85, AND SEQUENCE FROM N.A.  
 RX MEDLINE=94010323; PubMed=8406024; DOI=10.1016/0378-1119(93)90308-P;  
 RA Armour K.L., Harris W.J., Tempest P.R.;  
 RT "Cloning and expression in *Escherichia coli* of the cDNA encoding human  
 RT cardiac troponin I.";  
 RL Gene 131:287-292(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92035427; PubMed=1934363;  
 RA Hunkeler N.M., Kullman J., Murphy A.M.;  
 RT "Troponin I isoform expression in human heart.";  
 RL Circ. Res. 69:1409-1414(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96299735; PubMed=8661099; DOI=10.1006/geno.1996.0317;  
 RA Bhavsar P.K., Brand N.J., Yacoub M.H., Barton P.J.R.;  
 RT "Isolation and characterization of the human cardiac troponin I gene  
 RT (TNNT3).";  
 RL Genomics 35:11-23(1996).  
 RN [5]  
 RP PHOSPHORYLATION SITES SER-22 AND SER-23.  
 RX MEDLINE=9804271; PubMed=9346285;  
 RA Keane N.E., Quirk P.G., Gao Y., Patchell V.B., Perry S.V.,  
 RA Levine B.A.;  
 RT "The ordered phosphorylation of cardiac troponin I by the CAMP-  
 RT dependent protein kinase -- structural consequences and functional  
 RT implications.";  
 RL Eur. J. Biochem. 248:329-337(1997).  
 RN [6]  
 RP STRUCTURE BY NMR OF 147-163.  
 RX PubMed=10387074; DOI=10.1021/bi9901679;  
 RA Li M.X., Spyropoulos L., Sykes B.D.;  
 RT "Binding of cardiac troponin-I147-163 induces a structural opening in  
 RT human cardiac troponin-C.";  
 RL Biochemistry 38:8289-8298(1999).  
 RN [7]  
 RP STRUCTURE BY NMR OF 148-164 IN COMPLEX WITH CARDIAC TROPONIN C.  
 RX MEDLINE=22172844; PubMed=12060657; DOI=10.1074/jbc.M203896200;  
 RA Wang X., Li M.X., Sykes B.D.;  
 RT "Structure of the regulatory N-domain of human cardiac troponin C in  
 RT complex with human cardiac troponin I147-163 and bepridil.";  
 RL J. Biol. Chem. 277:31124-31133(2002).  
 RN [8]  
 RP VARIANTS CMH7 GLY-144 AND GLN-205.  
 RX MEDLINE=97385244; PubMed=9241277;  
 RA Kimura A., Harada H., Park J.-E., Nishi H., Satoh M., Takahashi M.,  
 RA Hiroi S., Sasaoka T., Ohbuchi N., Nakamura T., Koyanagi T.,  
 RA Hwang T.-H., Choo J., Chung K.-S., Hasegawa A., Nagai R., Okazaki O.,  
 RA Nakamura H., Matsuzaki M., Sakamoto T., Tushima H., Koga Y.,  
 RA Imaizumi T., Sasazuki T.;  
 RT "Mutations in the cardiac troponin I gene associated with hypertrophic  
 RT cardiomyopathy.";  
 RL Nat. Genet. 16:379-382(1997).  
 RN [9]  
 RP VARIANTS CMH7 SER-81 AND ASN-195.  
 RX MEDLINE=21673699; PubMed=11815426; DOI=10.1161/hc0402.102990;  
 RA Nimura H., Patton K.K., McKenna W.J., Soultis J., Maron B.J.,  
 RA Seidman J.G., Seidman C.E.;  
 RT "Sarcomere protein gene mutations in hypertrophic cardiomyopathy of  
 RT the elderly.";  
 RL Circulation 105:446-451(2002).  
 RN [10]  
 RP VARIANTS RCM GLN-143; TRP-144; THR-170; GLU-177; HIS-189 AND HIS-191.  
 RX MEDLINE=22419550; PubMed=12531876;  
 RA Mogensen J., Kubo T., Duque M., Uribe W., Shaw A., Murphy R.,

RA Gimeno J.R., Elliott P., McKenna W.J.;  
 RT "Idiopathic restrictive cardiomyopathy is part of the clinical  
 RT expression of cardiac troponin I mutations.";  
 RL J. Clin. Invest. 111:209-216(2003).  
 CC [1-] FUNCTION: Troponin I is the inhibitory subunit of troponin, the  
 CC thin filament regulatory complex which confers calcium-sensitivity  
 CC to striated muscle actomyosin ATPase activity.  
 CC [1-] SUBUNIT: Binds to actin and tropomyosin.  
 CC [1-] DISEASE: Defects in TNNT3 are the cause of familial hypertrophic  
 CC cardiomyopathy type 7 (CMH7) [MIM:191044]; also known as FHC type  
 CC 7. CMH7 is an autosomal dominant disorder characterized by  
 CC increased myocardial mass with myocyte and myofibrillar disarray.  
 CC [1-] DISEASE: Defects in TNNT3 are the cause of familial restrictive  
 CC cardiomyopathy (RCM) [MIM:115210]. RCM is an heart muscle disorder  
 CC characterized by impaired filling of the ventricles with reduced  
 CC volume in the presence of normal or near normal wall thickness and  
 CC systolic function. The disease may be associated with systemic  
 CC disease but is most often idiopathic.  
 CC [1-] SIMILARITY: Belongs to the troponin I family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X54163; CAA38102.1; ALT\_SEQ.  
 CC EMBL; M64247; AAA16157.1; -  
 CC EMBL; X90780; CAA62301.1; -  
 CC PIR; A61229; TPUHUC.  
 CC PDB; 1JUD; X-ray; C/F=30-162.  
 CC PDB; 1JLE; X-ray; C/F=30-208.  
 CC PDB; 1LXF; NMR; I=147-163.  
 CC PDB; 1MXL; NMR; I=147-163.  
 CC Genew; HGNC:11947; TNNT3.  
 CC MIM; 191044; -  
 CC MIM; 115210; -  
 CC GO; GO:0003861; C:troponin complex; TAS.  
 CC GO; GO:0008016; P:regulation of heart rate; TAS.  
 CC InterPro; IPR001978; Troponin.  
 CC Pfam; PF00992; Troponin; 1.  
 KW 3D-structure; Acetylation; Actin-binding; Cardiomyopathy;  
 KW Disease mutation; Muscle protein; Phosphorylation.  
 FT INIT\_MET 0 0  
 FT SITE 79 79 Involved in TNI-TNT interactions.  
 FT SITE 96 96 Involved in TNI-TNT interactions.  
 FT DOMAIN 31 78 Involved in binding TNC.  
 FT DOMAIN 128 148 Involved in binding TNC and actin.  
 FT MOD\_RES 1 1 N-acetyltalanine (By similarity).  
 FT MOD\_RES 22 22 Phosphoserine (by PKA).  
 FT MOD\_RES 23 23 Phosphoserine (by PKA).  
 FT VARIANT 81 81 P -> S (in CMH7).  
 FT VARIANT 143 143 /FTid=VAR\_016078.  
 FT VARIANT 143 143 L -> Q (in RCM).  
 FT VARIANT 144 144 /FTid=VAR\_016079.  
 FT VARIANT 144 144 R -> G (in CMH7).  
 FT VARIANT 144 144 /FTid=VAR\_007603.  
 FT VARIANT 144 144 R -> W (in RCM).  
 FT VARIANT 144 144 /FTid=VAR\_016080.  
 FT VARIANT 170 170 A -> T (in RCM).  
 FT VARIANT 170 170 /FTid=VAR\_016081.  
 FT VARIANT 177 177 K -> E (in RCM).  
 FT VARIANT 177 177 /FTid=VAR\_016082.  
 FT VARIANT 189 189 D -> H (in CMH7 and RCM).  
 FT VARIANT 189 189 /FTid=VAR\_016083.  
 FT VARIANT 191 191 R -> H (in RCM).  
 FT VARIANT 191 191 /FTid=VAR\_016084.  
 FT VARIANT 195 195 D -> N (in CMH7).  
 FT VARIANT 195 195 /FTid=VAR\_016085.  
 FT VARIANT 205 205 K -> Q (in CMH7).  
 FT VARIANT 205 205 /FTid=VAR\_007604.

RX	MEDLINE=77087072; PubMed=1008922;
RA	Grand R.J.A., Wilkinson J.M., Mole L.E.;
RT	"The amino acid sequence of rabbit cardiac troponin I.";
RL	Biochem. J. 159:633-641(1976).
RN	[2]
RP	REVISION.
RX	MEDLINE=78060292; PubMed=588250;
RA	Grand R.J.A., Wilkinson J.M.;
RT	"The amino acid sequence of rabbit slow-muscle troponin I.";
RL	Biochem. J. 167:183-192(1977).
RN	[3]
RN	SEQUENCE OF 1-36, AND PHOSPHORYLATION SITE SER-23.
RP	TISSUE=Heart;
RC	PubMed=2226863;
RA	Mittmann K., Jaquet K., Heilmeyer L.M. Jr.;
RT	"A common motif of two adjacent phosphoserines in bovine, rabbit and
RL	human cardiac troponin I.";
RN	PES Lett. 273:41-45(1990).
RN	[4]
RP	PHOSPHORYLATION SITE SER-22.
RX	MEDLINE=76267707; PubMed=958429;
RA	Solaro R.J., Moir A.J.G., Perry S.V.;
RT	"Phosphorylation of troponin I and the inotropic effect of adrenaline
RL	in the perfused rabbit heart.";
RN	Nature 262:615-617(1976).
CC	-I- FUNCTION: Troponin I is the inhibitory subunit of troponin, the
CC	thin filament regulatory complex which confers calcium-sensitivity
CC	to striated muscle actomyosin ATPase activity.
CC	-I- SUBUNIT: Binds to actin and tropomyosin.
CC	-I- PTM: Ser-22 is one of three sites in the region of residues 1-48
CC	that are phosphorylated by phosphorylase kinase.
CC	-I- SIMILARITY: Belongs to the troponin I family.
DR	PIR; A90296; TPRBIC.
DR	HSP; P19429; 1J1D.
DR	InterPro: IP001978; Troponin.
DR	pfam; PF00992; Troponin; 1.
KW	Acylation; Actin-binding; Direct protein sequencing; Muscle protein;
KW	Phosphorylation.
FT	MOD_RES 1 1 N-acetylalanine (By similarity) .
FT	MOD_RES 22 22 Phosphoserine (by PKH) .
FT	MOD_RES 23 23 Phosphoserine.
FT	SITE 80 80 Involved in TNI-TNT interactions.
FT	SITE 97 97 Involved in TNI-TNT interactions.
FT	DOMAIN 32 79 Involved in binding TNC.
FT	DOMAIN 129 150 Involved in binding TNC and actin.
FT	CONFLICT 5 5 R -> T.(in Ref. 3) .
FT	CONFLICT 17 17 Missing (in Ref. 1 and 2) .
FT	CONFLICT 21 26 RSSANY -> SD (in Ref. 1 and 2) .
SEQ	SEQUENCE 211 AA; A1S82683CS3B2FIC CRC64;
QY	Query Match 88.8%; Score 439.5; DB 1; Length 211;
Ddb	Best Local Similarity 90.3%; Pred. No. 2.2e-13;
QY	Matches 90; Conservative 2; Mismatches 6; Indels 1; Gaps 1
Ddb	1 ADGSSDAAREPAPAPIRRRS-NTRYATPEPHAKKGIKISASKLKQLTKLLQIAKQE 60   :                                 1 ADESRDAAGEARPAPAVRRRSSANRYATPEPHAKKIKISASRKIQKLTLMLQIAKQE 60
QY	61 LERAEERRKEGRALSTRCPLEAGLGFAELQDLCRQ 99   61 LERAEERRKEGRALSTRCPLEAGLGFAELQDLCRQ 99
Ddb	61 LERAEERRKEGRALSTRCPLEAGLGFAELQDLCRQ 99   61 LERAEERRKEGRALSTRCPLEAGLGFAELQDLCRQ 99
RESULT 5	
TRIC_MOUSE	STANDARD; PRT; 210 AA.
ID TRIC_MOUSE	
AC	P48787;
DT	01-FEB-1996 (Rel. 33, Created)
DDT	01-FEB-1996 (Rel. 33, Last sequence update)
DDT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Troponin I, cardiac muscle.
OS	Name=Tnni3; Mus musculus (Mouse).





[illegible]

[illegible]

FT DOMAIN 27 72 Involved in binding TNC.  
 SQ SEQUENCE 207 AA; 23470 MW; D785A518F93E4293 CRC64;  
 Query Match 60.9%; Score 301.5; DB 1; Length 207;  
 Best Local Similarity 67.4%; Pred. No. 1.9e-20;  
 Matches 62; Conservative 10; Mismatches 19; Indels 1; Gaps 1;  
 QY 9 AAREPRPAPAPRRSS-NYRAYATPHAKKSKISASRKLQKTLTLLQIAKQELERAE 67  
 DB 1 ABEERPPPPPLRRKSSSANYRYAYEPHAKKSKISASRKLQKTLTLLQIAKQELERAE 60  
 QY 68 RRGEKGRALSTRCPLELAGLGFAPLQDLQCRQ 99  
 DB 61 RAGEKQRLGELCPPELDGLGVAQLQELCRE 92  
 RESULT 13  
 ID Q63ZJO PRELIMINARY; PRT; 246 AA.  
 AC Q63ZJO;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT Initiative";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Skalek U., Smalley D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC082923; AAH82923.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 246 AA; 28333 MW; 685317D78F5D7730 CRC64;  
 Query Match 59.9%; Score 296.5; DB 2; Length 246;  
 Best Local Similarity 64.6%; Pred. No. 6.8e-20;

Matches 64; Conservative 10; Mismatches 18; Indels 7; Gaps 2;  
 QY 8 AAREPRPAPAP-----IRRSS-NYRAYATPHAKKSKISASRKLQKTLTLLQIAKQ 60  
 DB 28 APEPPKAPPPAAPPPLIRRRSSANYRAYATPQVKIKPKISASRKLQKSLMLQIAKAE 87  
 QY 61 LEREAEERGEKGRALSTRCPLELAGLGFAPLQDLQCRQ 99  
 DB 88 MEHEERERAREKERYLAECQPLQSLGSLSELQDLCRE 126  
 RESULT 14  
 TRIC\_XENLA  
 ID TRIC\_XENLA STANDARD; PRT; 243 AA.  
 AC PS0754;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Troponin I, cardiac muscle (troponin IC).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart muscle;  
 RX MEDLINE=95046865; PubMed=7958411; DOI=10.1006/dbio.1994.1265;  
 RA Drysdale T.A., Tonissen K.F., Patterson K.D., Crawford M.J.,  
 RA Krieg P.A.;  
 RT "Cardiac troponin I is a heart-specific marker in the Xenopus embryo:  
 RT expression during abnormal heart morphogenesis";  
 RL Dev. Biol. 165:432-441(1994).  
 CC -I- FUNCTION: Troponin I is the inhibitory subunit of troponin, the  
 CC thin filament regulatory complex which confers calcium-sensitivity  
 CC to striated muscle actomyosin ATPase activity.  
 CC -I- SUBUNIT: Binds to actin and tropomyosin.  
 CC -I- TISSUE SPECIFICITY: Heart.  
 CC -I- DEVELOPMENTAL STAGE: Expressed at all stages of development.  
 CC -I- SIMILARITY: Belongs to the troponin I family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; L25721; AAA65727.1; -  
 DR PIR; I51408; I51408.  
 DR HSSP; PI9429; IJID.  
 DR InterPro; IPR001978; Troponin.  
 DR Pfam; PF00992; Troponin; 1.  
 KW Actin-binding; Muscle protein.  
 FT INIT MET 0 0 By similarity.  
 FT DOMAIN 9 14 Poly-Glu.  
 FT DOMAIN 17 22 Poly-Glu.  
 FT DOMAIN 84 91 Poly-Glu.  
 FT SEQUENCE 243 AA; 28067 MW; A7CC018ACC26675 CRC64;  
 Query Match 59.5%; Score 294.5; DB 1; Length 243;  
 Best Local Similarity 62.6%; Pred. No. 1e-19;  
 Matches 62; Conservative 12; Mismatches 18; Indels 7; Gaps 2;  
 QY 8 AAREPRPAPAP-----IRRSS-NYRAYATPHAKKSKISASRKLQKTLTLLQIAKQ 60  
 DB 25 APEPPKAPPPAAPPPLIRRRSSANYRAYATPQVKIKPKISASRKLQKSLMLQIAKAE 84  
 QY 61 LEREAEERGEKGRALSTRCPLELAGLGFAPLQDLQCRQ 99  
 DB 85 MEHEERERAREKERYLAECQPLQSLGSLSELQDLCRE 123

```
RESULT 15
Q6YA69 PRELIMINARY; PRT; 238 AA.
ID Q6YA69
AC Q6YA69
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cardiac troponin I.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OC NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX PubMed=14745952; DOI=10.1002/dvdy.10434;
RA Warkman A.S., Atkinson B.G.;
RT "Amphibian cardiac troponin I gene's organization, developmental
RT expression, and regulatory properties are different from its mammalian
RT homologue."
RL Dev. Dyn. 229:275-288(2004).
DR EMBL; AY166834; AAC3937.1; -
DR GO; GO:0030484; C:muscle fiber; IEA.
DR InterPro; IPR001978; Troponin.
DR Pfam; PF00992; Troponin; 1.
SQ SEQUENCE 238 AA; 27415 MW; A2E1600D35594212 CRC64;

Query Match 59.3%; Score 293.5; DB 2; Length 238;
Best Local Similarity 59.4%; Pred. No. 1.3e-19;
Matches 57; Conservative 16; Mismatches 16; Indels 7; Gaps 1;

QY 11 EPPAPAPI-----RRSSNYRAYATEPHAKKKSASRKQLKLTLLQLAKOELER 63
Db 23 EKEPAPPVTVPLIRKKSANYRSYATEPHAKKPKITASRKQLKLGMLQLAKHEMSQ 82

QY 64 EAEERGERGRALSTRCPLELAGLGFALQDLCRQ 99
Db 83 EEARAQEKERVLAERCEPLQSLSLSHLDNCRE 118
```

Search completed: August 30, 2005, 12:11:39  
Job time : 170 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 11:49:21 ; Search time 165 Seconds  
(without alignments)  
232.056 Million cell updates/sec

Title: US-09-941-997-2

Perfect score: 495

Sequence: 1 MADGSDAAREPRAPAPR.....COFLEAGLFAELQDLCRQ 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	100.0	99	3 AAY87943	Aay87943 Human tro
2	495	100.0	203	6 ABO14732	Abol14732 Novel hum
3	495	100.0	210	2 AAB12185	Aab12185 Human tro
4	495	100.0	210	4 ADT02432	Adt02432 Human Tro
5	495	100.0	210	6 ABO14735	Abol14735 Novel hum
6	495	100.0	210	7 ADJ68246	Adj68246 Human hea
7	495	100.0	210	7 ADJ70547	Adj70547 Human hea
8	495	100.0	211	2 AAY03179	Aay03179 Human car
9	495	100.0	212	2 AAW94061	Aaw94061 Cardiac t
10	495	100.0	216	2 AAW41573	Aaw41573 Modified
11	495	100.0	216	2 AAW72758	Aaw72758 Modified
12	495	100.0	216	3 AAY91087	Aay91087 Recombina
13	495	100.0	216	7 ADG14208	Adg14208 Human tro
14	495	100.0	222	2 AAW41570	Aaw41570 Modified
15	495	100.0	222	6 ABO14731	Abol14731 Novel hum
16	495	100.0	371	7 ADG14211	Adg14211 Human tro
17	495	100.0	390	2 AAY25115	Aay25115 Human car
18	495	100.0	390	7 ADG14206	Adg14206 Human Tro
19	491	99.2	226	2 AAW18054	Aaw18054 Recombina
20	491	99.2	226	2 AAY03174	Aay03174 Recombina
21	491	99.2	226	2 AAY03168	Aay03168 Recombina
22	491	99.2	319	2 AAW41572	Aaw41572 Human car
23	491	99.2	372	2 AAW41571	Aaw41571 Cardiac t
24	490	99.0	209	8 ADO03924	Ado03924 Human ful
25	487	98.4	203	6 ABO14734	Abol14734 Novel hum

#### ALIGNMENTS

##### RESULT 1

AAY87943

ID AAY87943 standard; protein; 99 AA.

XX AC AAY87943;

DT 11-SEP-2000 (first entry)

DE Human troponin I protein.

XX Troponin I; human; cardiac; TnI; detection; myocardial infarction;

KW immunodetection; angina; dyspepsia.

XX Homo sapiens.

XX Key Location/Qualifiers  
FT Region 20..30

FT Region /note= "specifically claimed in Claim 9"

FT Region 95..115  
FT Region /note= "Specifically claimed in claim 9"

XX WO200023585-A1.

XX 27-APR-2000.

XX 19-OCT-1999; 99WO-IB001716.

XX 21-OCT-1998; 98US-00176546.

XX (SPEC-) SPECTRAL DIAGNOSTICS INC.

XX Shi Q, Liu S, Ling M;

XX WPI; 2000-422482/36.

XX N-ESDB; AAA39659.

XX New polypeptide useful in assays to identify troponin I associated with cardiac disorders, corresponds to N terminal fragment of human cardiac troponin I.

XX Claim 3; Page 30-31; 34pp; English.

XX This invention describes a novel isolated polypeptide (I) corresponding to an N-terminal fragment of human cardiac troponin I consisting of about 95 to 115 amino acids. Antibodies raised against (I) are useful for the immunodetection of human cardiac troponin I in a bodily fluid, a vital test for suspected acute myocardial infarction, angina and dyspepsia. (I) are used as controls and calibrators for assays which measure the

Aaw18053 Recombina  
Aay03176 Human car  
Aay03169 Human car  
Aaw94064 Cardiac t  
Aay03175 Human car  
Aay03167 Human car  
Abg23116 Novel hum  
Aaw94063 Cyanogen  
Ado03928 Mouse ful  
Abp98855 Human str  
Ado03916 Rat full  
Abg23117 Novel hum  
Ado03927 Bovine fu  
Aaw02286 Human tro  
Aaw94062 Cardiac t  
Aay03180 Human car  
Ado03925 Rabbit fu  
Adt02426 Human Tro  
Adt02428 Human Tro  
Adel13683 Human car

26 486 98.2 153 2 AAW18053  
27 486 98.2 153 2 AAY03176  
28 486 98.2 153 2 AAY03169  
29 486 98.2 208 2 AAW94064  
30 486 98.2 209 2 AAY03175  
31 486 98.2 209 2 AAY03167  
32 477.5 96.5 162 4 ABG23116  
33 444 89.7 150 2 AAW94063  
34 435.5 88.0 210 8 ADO03928  
35 435.5 88.0 211 6 ABP98855  
36 433.5 87.6 210 8 ADO03916  
37 423.5 85.6 229 4 ABG23117  
38 413 83.4 211 8 ADO03927  
39 397 80.2 80 2 AAW02286  
40 397 80.2 80 2 AAW94062  
41 395 79.8 80 2 AAY03180  
42 394 79.6 206 8 ADO03925  
43 356 71.9 247 4 ADT02426  
44 356 71.9 264 4 ADT02428  
45 331 66.9 178 8 ADS13683

CC fragments in biological samples. (I) may be used as an affinity matrix  
 CC for purifying antibodies from an animal immunized with native troponin I  
 CC to isolate those antibodies recognizing epitopes of the fragment. Prior  
 CC art assays use different methodologies and components so the  
 CC calibrators/controls cannot be used interchangeably among assays. Also,  
 CC troponin I in vivo undergoes proteolytic degradation by enzymes present  
 CC in the body. (I) is more resistant to proteolysis and is readily  
 CC detectable by components of different assays. This sequence represents  
 CC the human cardiac troponin I which is described in the method of the  
 CC invention  
 XX

SQ Sequence 99 AA;  
 Query Match 100.0%; Score 495; DB 3; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-49;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATPHAKKSKISASRKLQTLTLLQIAKQE 60  
 DB 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATPHAKKSKISASRKLQTLTLLQIAKQE 60  
 QY 61 LEREAEEREGKGRALSTRCQPLELAGLGFAPLQDLCRQ 99  
 DB 61 LEREAEEREGKGRALSTRCQPLELAGLGFAPLQDLCRQ 99

RESULT 2  
 ABO14732  
 ID ABO14732 standard; protein; 203 AA.  
 AC ABO14732;  
 XX  
 XX 25-AUG-2003 (first entry)  
 XX Novel human protein #105.  
 DE Human; NOV; gene therapy; endocrine related disease; diabetes;  
 KW Metabolism-related disease; obesity; central nervous system disorder;  
 KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;  
 KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;  
 KW psoriasis; allergy; lupus erythematosus; asthma; cancer;  
 KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;  
 KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;  
 KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;  
 KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;  
 KW stroke; infection.

XX Homo sapiens.  
 OS  
 XX WO2003023002-A2.  
 XX  
 XX 20-MAR-2003.  
 XX  
 XX 09-SEP-2002/ 2003WO-US028539.  
 XX  
 XX 07-SEP-2001/ 2001US-0318120P.  
 XX 07-SEP-2001/ 2001US-0318130P.  
 XX 10-SEP-2001/ 2001US-0318430P.  
 XX 17-SEP-2001/ 2001US-0322636P.  
 XX 17-SEP-2001/ 2001US-0322781P.  
 XX 17-SEP-2001/ 2001US-0322816P.  
 XX 17-SEP-2001/ 2001US-0322817P.  
 XX 19-SEP-2001/ 2001US-0323519P.  
 XX 20-SEP-2001/ 2001US-0323631P.  
 XX 20-SEP-2001/ 2001US-0323636P.  
 XX 25-SEP-2001/ 2001US-0324969P.  
 XX 26-SEP-2001/ 2001US-0325091P.  
 XX 26-SEP-2001/ 2001US-0324990P.  
 XX 17-APR-2002/ 2002US-0373212P.  
 XX 06-SEP-2002/ 2002US-00236177.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX

PI Spytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;  
 PI Gerlach VL, Vernet CM, Ellerman K, Berghs C, Rothenberg ME, Guo X;  
 PI Shimketa RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;  
 PI Rieser DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;  
 PI Lepley DM, Edinger SR, Burgess CE;  
 XX WPI; 2003-313242/30.  
 DR N-PSDB; ACD19425.  
 XX  
 XX New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)  
 PT and polynucleotides, useful in gene therapy, e.g. for treating or  
 PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,  
 PT stroke or infections.

Claim 1; Page 311; 586pp; English.

XX The invention describes a new isolated polypeptide (NOVX). The NOVX  
 CC polypeptide, nucleic acid and antibody are useful as therapeutics,  
 CC particularly in the manufacture of a medicament for treating a syndrome  
 CC associated with a human disease, which includes a pathology associated  
 CC with NOVX polypeptide. The DNA encoding the protein is useful in gene  
 CC therapy for treating the disease or condition. In particular, the NOVX  
 CC polypeptide or polynucleotide is useful for treating endocrine/  
 CC metabolism-related diseases (e.g. obesity or diabetes), central nervous  
 CC system disorders (e.g. Alzheimer's disease, Parkinson's disease,  
 CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune  
 CC and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,  
 CC asthma, inflammatory bowel disease, rheumatoid arthritis or  
 CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,  
 CC prostate or brain cancers, or melanoma), liver diseases (e.g. liver  
 CC cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),  
 CC haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).  
 CC These are also useful in developing powerful assay system for functional  
 CC analysis of various human disorders, as well as in diagnostic  
 CC applications, and for monitoring the effects of drugs during clinical  
 CC trials. This is the amino acid sequence of a novel human NOV protein

SQ Sequence 203 AA;

Query Match 100.0%; Score 495; DB 6; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATPHAKKSKISASRKLQTLTLLQIAKQE 60  
 DB 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATPHAKKSKISASRKLQTLTLLQIAKQE 60  
 QY 61 LEREAEEREGKGRALSTRCQPLELAGLGFAPLQDLCRQ 99  
 DB 61 LEREAEEREGKGRALSTRCQPLELAGLGFAPLQDLCRQ 99

RESULT 3  
 AAB12185  
 ID AAB12185 standard; protein; 210 AA.  
 XX  
 XX AAB12185;  
 XX  
 XX 10-NOV-2000 (first entry)  
 XX Human troponin I cardiac isoform (cTnI).  
 XX Human; troponin I; cTnI; muscle; acute myocardial infarction;  
 XX protein subunit stabilisation.  
 XX Homo sapiens.  
 XX US6072040-A.  
 XX 06-JUN-2000.  
 XX 15-OCT-1997; 97US-00950925.  
 XX  
 XX

PR 15-OCT-1996; 96US-00730111.  
 XX (MED-1) MEDICAL ANALYSIS SYSTEMS INC.  
 XX Sinter E, Dave KI, Botyanszki J;  
 XX WPI; 1998-251059/22.  
 DR N-PSDB; AAA62127.  
 XX  
 XX Stabilising individual sub-units of multimeric protein by attaching to  
 PT polymer - particularly cardiac troponin sub-units for use as controls in  
 PT immunoassays for diagnosis of acute myocardial infarct.  
 XX  
 XX Disclosure; Col 13-16; 17pp; English.  
 XX  
 XX Troponin is a three-subunit complex of troponin I, T and C. The troponin  
 CC complex is involved in the calcium-sensitive switch that regulates actin  
 CC and myosin interaction in striated muscles. The present sequence is the  
 CC protein sequence of the cardiac isoform of troponin I. ctni is a specific  
 CC marker for the diagnosis of acute myocardial infarction. The ctni protein  
 CC subunit may be stabilised by covalent conjugation to polymers, where a  
 CC solution of ctni is mixed with an active polymer allowing a ctni-polymer  
 CC conjugate to be formed. Stabilised conjugates of ctni are useful as  
 CC control reagent compositions for immunoassays. The stabilising effect of  
 CC conjugation allows the individual subunit to be stored in liquid medium  
 CC for longer periods of time than an equivalent unconjugated or "free"  
 CC individual subunit  
 XX  
 XX Sequence 210 AA;  
 SQ  
 Query Match 100.0%; Score 495; DB 2; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKQLTKLLQIAKOE 60  
 DB 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKQLTKLLQIAKOE 60  
 QY 61 LEREAEERGERGKRALSTRCQPLELAGLGFAPLQDLCRQ 99  
 DB 61 LEREAEERGERGKRALSTRCQPLELAGLGFAPLQDLCRQ 99  
 RESULT 4  
 ADT02432  
 ID ADT02432 standard; protein; 210 AA.  
 XX  
 XX ADT02432;  
 XX  
 XX 02-DEC-2004 (first entry)  
 DT Human Troponin I subunit.  
 DE  
 XX Human; Troponin I; Troponin C; antigen; myocardial infarction; cardiac.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US6475785-B1.  
 PN  
 XX 05-NOV-2002.  
 PD  
 XX 05-AUG-1999; 99US-00368819.  
 PF  
 PR 18-DEC-1997; 97US-00993380.  
 PR 21-OCT-1998; 98US-00176546.  
 XX  
 XX (SPEC-) SPECTRAL DIAGNOSTICS INC.  
 PA  
 XX Shi Q, Liu S, Ling M;  
 PI  
 XX WPI; 2001-202771/20.  
 DR  
 XX Single-chain polypeptides comprising an N-terminal fragment of cardiac

PT troponin I and cardiac troponin C, useful as controls or calibrators for  
 PT troponin assays.  
 XX  
 XX Disclosure; SEQ ID NO 8; 11pp; English.  
 XX  
 XX The invention relates to a single-chain polypeptide comprising a N-  
 CC terminal fragment of cardiac troponin I and a cardiac troponin C. The  
 CC presence of cardiac troponin subunits (I, C or T) in the bloodstream is a  
 CC marker for myocardial infarction. Also included are a polynucleotide  
 CC encoding the polypeptide, a replicatable cloning or expression vehicle  
 CC comprising the polynucleotide; a host cell transformed with the  
 CC expression vehicle, a composition (comprising the polypeptide) for use as  
 CC a control or calibrator for a troponin I assay and quantitating troponin  
 CC I in a sample (by measuring troponin I in the sample, measuring the  
 CC fusion protein in a standard having a known quantity of troponin I, and  
 CC correlating the troponin I measured in the sample with the known quantity  
 CC of troponin I measured in the standard, to provide the quantity of  
 CC troponin I in the sample). The single-chain polypeptide is useful as a  
 CC control or calibrator for a troponin I assay and for affinity  
 CC purification of troponin antibodies. The present sequence represents  
 CC human troponin I subunit. NOTE: The present sequence is included in the  
 CC sequence listing but is not mentioned anywhere else in the specification.  
 CC The identity of the sequence was determined by the indexer via BLAST  
 CC searching and by comparison to ADT02426, where the sequence was found to  
 CC be 100% identical to human Troponin I and matched the N-terminus of  
 CC ADT02426.  
 XX  
 XX Sequence 210 AA;  
 SQ  
 Query Match 100.0%; Score 495; DB 4; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKQLTKLLQIAKOE 60  
 DB 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKQLTKLLQIAKOE 60  
 QY 61 LEREAEERGERGKRALSTRCQPLELAGLGFAPLQDLCRQ 99  
 DB 61 LEREAEERGERGKRALSTRCQPLELAGLGFAPLQDLCRQ 99  
 RESULT 5  
 AB014735  
 ID AB014735 standard; protein; 210 AA.  
 XX  
 XX AB014735;  
 XX  
 XX 25-AUG-2003 (first entry)  
 DT Novel human protein #108.  
 DE  
 XX Human; NOV; gene therapy; endocrine related disease; diabetes;  
 KW metabolism-related disease; obesity; central nervous system disorder;  
 KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;  
 KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;  
 KW psoriasis; allergy; lupus erythematosus; asthma; cancer;  
 KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;  
 KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;  
 KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;  
 KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;  
 KW stroke; infection.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2003023002-A2.  
 PN  
 XX 20-MAR-2003.  
 PD  
 XX 09-SEP-2002; 2002WO-US028539.  
 PF  
 XX 07-SEP-2001; 2001US-0318120P.  
 PR 07-SEP-2001; 2001US-0318130P.  
 PR



PR 10-SEP-2001; 2001US-0318430P.  
 PR 17-SEP-2001; 2001US-0322636P.  
 PR 17-SEP-2001; 2001US-0322781P.  
 PR 17-SEP-2001; 2001US-0322816P.  
 PR 17-SEP-2001; 2001US-0322817P.  
 PR 19-SEP-2001; 2001US-0323519P.  
 PR 20-SEP-2001; 2001US-0323631P.  
 PR 20-SEP-2001; 2001US-0323636P.  
 PR 25-SEP-2001; 2001US-0324969P.  
 PR 25-SEP-2001; 2001US-0325091P.  
 PR 26-SEP-2001; 2001US-0324990P.  
 PR 17-APR-2002; 2002US-0373212P.  
 PR 06-SEP-2002; 2002US-00236177.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Spytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;  
 PI Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;  
 PI Shinkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;  
 PI Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;  
 PI Lepley DM, Edinger SR, Burgess CE;  
 XX  
 DR WPI; 2003-313242/30.  
 DR N-PSDB; ACD19428.  
 XX  
 PT New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)  
 PT and polynucleotides, useful in gene therapy, e.g. for treating or  
 PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,  
 PT stroke or infections.

Claim 1; Page 312; 596pp; English.

The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polynucleotide is useful for treating endocrine/metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus, asthma, inflammatory bowel disease, rheumatoid arthritis or osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (emphysema or obstructive pulmonary disease), haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications, and for monitoring the effects of drugs during clinical trials. This is the amino acid sequence of a novel human NOV protein

Sequence 210 AA;

Query Match 100.0%; Score 495; DB 6; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPARRSSNRYAYATPHAKKSKISASRKLQKTLTLLQIAKQE 60  
 Db 1 MADGSSDAAREPRPAPAPARRSSNRYAYATPHAKKSKISASRKLQKTLTLLQIAKQE 60  
 Qy 61 LERAEERERGERALSTRCPLEAGLGFAGLQDLCRQ 99  
 Db 61 LERAEERERGERALSTRCPLEAGLGFAGLQDLCRQ 99

RESULT 6

ADJ68246

ID ADJ68246 standard; protein; 210 AA.

XX AC

ADJ70547

XX 06-MAY-2004 (first entry)  
 DT Human heat mitochondrial protein as a therapeutic target SeqID52.  
 XX  
 DE Mitochondrial; human; screening assay; diabetes mellitus;  
 XX Huntington's disease; osteoarthritis;  
 KW Leber's hereditary optic neuropathy; LHON;  
 KW Mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;  
 KW osteopathic; ophthalmological; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003087768-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 04-APR-2003; 2003WO-US010870.  
 XX  
 PR 12-APR-2002; 2002US-0372843P.  
 PR 17-JUN-2002; 2002US-0369987P.  
 PR 20-SEP-2002; 2002US-0412418P.  
 XX  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 XX  
 FI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
 FI Warnock DE;  
 XX  
 DR WPI; 2003-845369/78.  
 XX  
 PT Identifying a mitochondrial target for drug screening assays and for  
 PT treating diseases associated with altered mitochondrial function,  
 PT comprises detecting a modified polypeptide in a sample and correlating  
 PT with the disease.  
 XX  
 PS Claim 1; SEQ ID NO 52; 180pp; English.  
 XX  
 CC This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, nontropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cytostatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.

Sequence 210 AA;

Query Match 100.0%; Score 495; DB 7; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADGSSDAAREPRPAPAPARRSSNRYAYATPHAKKSKISASRKLQKTLTLLQIAKQE 60  
 Db 1 MADGSSDAAREPRPAPAPARRSSNRYAYATPHAKKSKISASRKLQKTLTLLQIAKQE 60  
 Qy 61 LERAEERERGERALSTRCPLEAGLGFAGLQDLCRQ 99  
 Db 61 LERAEERERGERALSTRCPLEAGLGFAGLQDLCRQ 99

RESULT 7

ADJ70547

ADJ70547 standard; protein; 210 AA.  
 ADJ70547;  
 06-MAY-2004 (first entry)  
 Human heat mitochondrial protein as a therapeutic target SeqID2353.  
 mitochondrial; human; screening assay; diabetes mellitus;  
 Huntington's disease; osteoarthritis;  
 Leber's hereditary optic neuropathy; LHON;  
 mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
 osteopathic; ophthalmological; cytostatic.  
 Homo sapiens.  
 WO2003087768-A2.  
 23-OCT-2003.  
 04-APR-2003; 2003WO-US010870.  
 12-APR-2002; 2002US-0372843P.  
 17-JUN-2002; 2002US-0389987P.  
 20-SEP-2002; 2002US-0412418P.  
 (MITO-) MITOKOR.  
 (BUCK-) BUCK INST AGE RES.  
 Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
 Warnock DE;  
 WPI; 2003-845369/78.  
 Identifying a mitochondrial target for drug screening assays and for  
 treating diseases associated with altered mitochondrial function,  
 comprises detecting a modified polypeptide in a sample and correlating  
 with the disease.  
 Claim 1; SEQ ID NO 2353; 180pp; English.  
 This invention relates to novel mitochondrial targets that can be used  
 for therapeutic intervention in treating a disease associated with  
 altered mitochondrial function. Specifically, it refers to a method for  
 identifying proteins of the human heart mitochondrial proteome that are  
 useful for drug screening assays, as well as therapeutic targets. The  
 present invention describes a method for identifying such proteins that  
 can be used in the treatment of various diseases associated with altered  
 mitochondrial function including diabetes mellitus, Huntington's disease,  
 osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 compositions have neuroprotective, nootropic, antidiabetic,  
 anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 cytostatic activities. This polypeptide sequence is a human heart  
 mitochondrial protein of the invention.

Query Match 100.0%; Score 495; DB 7; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATPEPHAKKSKISASRKLQKTLTLLQIAKOE 60  
 DB 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATPEPHAKKSKISASRKLQKTLTLLQIAKOE 60  
 QY 61 LEREAEEREGKRALSTRCQPLELAGLGFALQDLQCRQ 99  
 DB 61 LEREAEEREGKRALSTRCQPLELAGLGFALQDLQCRQ 99

Sequence 210 AA;

RESULT 8  
 AAY03179  
 ID AAY03179 standard; peptide; 211 AA.  
 XX  
 AC AAY03179;  
 XX  
 DT 15-JUN-1999 (first entry)  
 XX  
 DE Human cardiac troponin I fragment.  
 XX  
 KW Human; cardiac troponin I; TnI; diagnostic calibrator; troponin assay.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9854219-A1.  
 XX  
 PD 03-DEC-1998.  
 XX  
 PF 21-MAY-1998; 98WO-US010518.  
 XX  
 PR 29-MAY-1997; 97US-00865468.  
 PR 13-JUN-1997; 97US-00874566.  
 PR 22-JUL-1997; 97US-00898649.  
 XX  
 PA (MEDI-) MEDICAL ANALYSIS SYSTEMS INC.  
 XX  
 PI Moriana N;  
 XX  
 DR WPI; 1999-059811/05.  
 XX  
 PT New compositions comprising complexes of cardiac troponin I or T - useful  
 PT as diagnostic calibrators, or controls or reference material for TnI or  
 PT TnT.  
 XX  
 PS Disclosure; Page 18; 50pp; English.  
 XX  
 CC This sequence represents a human cardiac troponin I (TnI) fragment. The  
 CC invention relates to compositions used in an assay for determining the  
 CC presence/concentration of TnI or TnT. The compositions comprise a complex  
 CC of either/both TnI or TnT (including fragments), covalently bound to TnC  
 CC (including fragments) or each other. The complexes are useful as  
 CC diagnostic calibrators or controls in methods for assaying each troponin  
 CC (especially TnI and TnT), and they are also useful as reference materials  
 CC for TnI and TnT. The compositions possess higher stability and/or  
 CC immunoreactivity over prior art complexes and analytes  
 XX  
 SQ Sequence 211 AA;  
 Query Match 100.0%; Score 495; DB 2; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATPEPHAKKSKISASRKLQKTLTLLQIAKOE 60  
 DB 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATPEPHAKKSKISASRKLQKTLTLLQIAKOE 60  
 QY 61 LEREAEEREGKRALSTRCQPLELAGLGFALQDLQCRQ 99  
 DB 61 LEREAEEREGKRALSTRCQPLELAGLGFALQDLQCRQ 99

RESULT 9  
 AAW94061  
 ID AAW94061 standard; peptide; 212 AA.  
 XX  
 AC AAW94061;  
 XX  
 DT 09-APR-1999 (first entry)  
 XX  
 DE Cardiac troponin I (cTnI) protein fragment.  
 XX  
 KW Myoglobin; troponin; anoxia; antioxidant; clinical assay; TnI; TnT; TnC;

KW calcium; stabilise; cardiac marker; cardiac; lyophilisate;  
 KW cardiac troponin I; cTnI; human; bovine.

OS Homo sapiens.  
 OS Bos sp.

PN WO9856900-A1.

PD 17-DEC-1998;

PF 09-JUN-1998/ 98WO-US011809.

PR 13-JUN-1997/ 97US-00874566.

PR 22-JUL-1997; 97US-00898538.

PA (MEDI-) MEDICAL ANALYSIS SYSTEMS INC.

PI Palmer DD, Morjana N;

DR WPI; 1999-070321/06.

XX Stabilised control solutions for clinical analysis of cardiac markers -  
 PT containing one or more of myoglobin, troponins, creatine kinase and  
 PT carbonic anhydrase, for diagnosis of cardiac function.

PS Disclosure; Page 16; 55pp; English.

CC The invention relates to stabilised compositions for use in clinical  
 CC assays. Composition to stabilise myoglobin consists of an aqueous  
 CC buffered solution of myoglobin and can be used for maintaining anoxia and  
 CC antioxidants. Composition for clinical assays to stabilise troponin I  
 CC (TnI) or troponin T (TnT) comprises (i) TnI or TnT, (ii) TnC (at least  
 CC equimolar to (i)) and (iii) calcium ions; wherein the composition is  
 CC stabilised through a heat treatment process. The compositions are used to  
 CC analyse for various cardiac markers (for diagnosis of cardiac function),  
 CC specifically as a control for assay of myoglobin and as control or stock  
 CC solution for assay of Tn. In these formulations, the cardiac proteins are  
 CC stabilised, e.g. myoglobin is stable for at least 1 year at 4 deg. C. In  
 CC the Tn-containing compositions, the heating step and the use of excess  
 CC TnC both contribute to stability, and several different cardiac proteins  
 CC may be stabilised in the same solution (which may also be stored as  
 CC lyophilisate). The present sequence represents cardiac troponin I (cTnI)  
 CC fragment that can be recombinantly obtained from human cTnI or bovine  
 CC cTnI

XX Sequence 212 AA;

Query Match 100.0%; Score 495; DB 2; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATPHAKKSKISASRKLQKTLTLLQIAKOE 60  
 DB 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATPHAKKSKISASRKLQKTLTLLQIAKOE 60  
 QY 61 LERAEERERGGKRALSTRCPQLELAGLGFAGLQDLQCRQ 99  
 DB 61 LERAEERERGGKRALSTRCPQLELAGLGFAGLQDLQCRQ 99

RESULT 10

AAW41573

ID AAW41573 standard; protein; 216 AA.

XX AAW41573;

XX 22-JUN-1998 (first entry)

XX Modified human cardiac troponin I HcTnI-(HL)3.

XX Troponin I; immunoassay; assay; analysis; human; cardiac muscle;  
 KW skeletal muscle; injury; myocardial infarction; diagnosis; HcTnI-(HL)3.

OS Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Protein 1..210  
 FT /label= HcTnI  
 FT Peptide 211..216  
 FT /label= (HL)3  
 FT /note= "(Claim 23)"

XX WO9799132-A1.

XX 23-OCT-1997.

XX 14-APR-1997; 97WO-US006147.

XX 16-APR-1996; 96US-0015772P.

XX 11-APR-1997; 97US-00833743.

XX (UYMI-) UNIV MIAMI.

XX Potter JD;

XX WPI; 1998-062676/06.

XX N-PSDB; AAV04230.

XX Immunoassay of mammalian troponin using stable standard for comparison -  
 PT specifically acid-dialysed solution or its lyophilisate used for  
 PT diagnosis of cardiac or skeletal muscle damage.

XX Example 5; Page 74-75; 94pp; English.

CC This polypeptide comprises a C-terminally modified cardiac troponin I  
 CC protein, designated HcTnI-(HL)3, comprising human cardiac troponin I  
 CC (HcTnI) modified to add an alternating 3 histidine 3 leucine tag (see  
 CC AAW41569). This modification alters the isoelectric point of the protein,  
 CC thereby improving its solubility and stability. A polynucleotide (see  
 CC AAV04230) encoding the modified HcTnI was produced by PCR amplification  
 CC of a HcTnI cDNA template, and was inserted into vector pET 11d to allow  
 CC expression of HcTnI-(HL)3 in Escherichia coli transformants. The  
 CC invention provides an assay for measuring mammalian, preferably human,  
 CC troponin in a patient sample. The assay involves comparing the level in  
 CC the sample with a novel troponin protein standard. This is a storage  
 CC stable, soluble troponin, a functional fragment of the troponin, a  
 CC modified troponin or its functional fragment, a troponin fusion protein  
 CC or a hetero-multimeric troponin complex (see AAW41570-75). The method is  
 CC used to monitor changes in the level of human troponin, particularly for  
 CC diagnosis of diseases involving damage to heart or skeletal muscle, e.g.  
 CC acute myocardial infarction. It may also be used to study normal and  
 CC pathological functions of troponin-expressing tissues

XX Sequence 216 AA;

Query Match 100.0%; Score 495; DB 2; Length 216;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATPHAKKSKISASRKLQKTLTLLQIAKOE 60  
 DB 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATPHAKKSKISASRKLQKTLTLLQIAKOE 60  
 QY 61 LERAEERERGGKRALSTRCPQLELAGLGFAGLQDLQCRQ 99  
 DB 61 LERAEERERGGKRALSTRCPQLELAGLGFAGLQDLQCRQ 99

RESULT 11

AAW72758

ID AAW72758 standard; protein; 216 AA.

XX AAW72758;

XX 13-JAN-1999 (first entry)

XX	Modified human cardiac troponin I.
DE	
XX	
XX	Human cardiac troponin I; troponin T; modified; antigen;
KW	stable troponin subunit; cardiac disorder; myocardial damage;
KW	heart attack.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FN	US5834210-A.
PD	10-NOV-1998.
XX	
PF	31-OCT-1997; 97US-00961858.
XX	
PR	23-MAY-1997; 97US-00862613.
XX	
PA	(SPEC-) SPECTRAL DIAGNOSTICS INC.
XX	
PI	Shi Q, Liu S;
XX	
DR	WPI; 1999-008702/01.
DR	N-PSDB; AAV67262.
XX	
FT	Recombinant modified human cardiac troponin I and complexes with troponin
PT	T and C - for use in assays to determine levels of these proteins, as
PT	control values in determining extent of cardiac damage e.g. in heart
PT	attacks.
XX	
PS	Claim 2; Fig 1; 16pp; English.
XX	
CC	The present sequence represents modified human cardiac troponin I.
CC	Expression in Escherichia coli of the modified troponin I is increased
CC	compared to that of the native sequence. The modified troponin I consists
CC	of the native troponin I protein sequence with an N-terminal extension of
CC	5-8 residues, including an N-terminal methionine. The present invention
CC	describes troponin protein complexes which are useful for the
CC	determination of myocardial damage. Troponin I and troponin T have been
CC	found to be highly specific markers for cardiac disorders, especially
CC	heart attacks. They must be complexed with troponin C to form a stable
CC	structure, which is difficult to isolate. Recombinant preparation of the
CC	trimeric structure allows sufficient quantities to be obtained, so that
CC	assays can be performed to accurately determine quantification of
CC	troponin complex levels for e.g. control values. The complex can also be
CC	used as an antigen to raise antibodies
XX	
SQ	Sequence 216 AA;
	Query Match 100.0%; Score 495; DB 2; Length 216;
	Best Local Similarity 100.0%; Pred. No. 1.1e-48;
	Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MADGSSDAAREPRAPAPIRRSSNYRAYATEPHAKKSKISASRKQLKTLIIQIAKQE 60
Db	7 MADGSSDAAREPRAPAPIRRSSNYRAYATEPHAKKSKISASRKQLKTLIIQIAKQE 66
QY	61 LERAEERRGKGRALSTRCQPLELAGIGFAELQDLCRQ 99
Db	67 LERAEERRGKGRALSTRCQPLELAGIGFAELQDLCRQ 105
	RESULT 12
AAAY91087	
ID	AAAY91087 standard; protein; 216 AA.
XX	
AC	AAAY91087;
XX	
DT	08-SEP-2000 (first entry)
XX	
DE	Recombinant modified human cardiac troponin I SEQ ID NO:5.
XX	
KW	Human; cardiac troponin I; cardiac troponin T; modified.

XX 10-DEC-1999; 99US-00458770.  
XX (SHIQ/) SHI Q.  
PA (SONG/) SONG Q.  
XX SHI Q. Song Q;  
XX PI SHI Q.  
XX WPI; 2003-898591/82.  
DR N-PSDB; ADG14207.  
XX  
XX New genetic sequence that codes for a single-chain polypeptide comprises  
PT cardiac troponin I and troponin C useful for purifying proteins and other  
PT substances including antibodies with an affinity for binding troponin I  
PT and troponin C.  
XX  
XX Disclosure; SEQ ID NO 6; 18pp; English.  
XX  
XX The invention relates to a genetic sequence, which codes for a single-  
CC chain polypeptide, comprising cardiac troponin I and troponin C  
CC (appearing as ADG14205 encoding ADG14206) separated by a synthetic  
CC linker. Also included are a replicatable cloning or expression vehicle  
CC comprising the novel genetic sequence, a host cell transformed with the  
CC vehicle, an Escherichia coli transformed with the replicatable cloning or  
CC expression vehicle and a single-chain polypeptide comprising cardiac  
CC troponin I and C. The genetic sequence is useful for purifying proteins  
CC and other substances including antibodies with an affinity for binding  
CC troponin I and troponin C, for use in diagnostic tests for myocardial  
CC infarction (heart attack). The present sequence represents troponin C.  
XX  
XX Sequence 216 AA;  
SQ  
Query Match 100.0%; Score 495; DB 7; Length 216;  
Best Local Similarity 100.0%; Pred. No. 1.1e-48;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MADSSDAAREPRPAPAPIRRRSSNYRAYATPEPHAKKSKISASRKLQKLTLLQIAKOE 60  
DB 7 MADSSDAAREPRPAPAPIRRRSSNYRAYATPEPHAKKSKISASRKLQKLTLLQIAKOE 66  
OY 61 LERAEEREGKGRALSTRCOPLELAGLGFAPLQDLCRQ 99  
DB 67 LERAEEREGKGRALSTRCOPLELAGLGFAPLQDLCRQ 105  
RESULT 14  
AAW41570  
ID AAW41570 standard; protein; 222 AA.  
XX  
XX AAW41570;  
XX  
XX 22-JUN-1998 (first entry)  
XX Modified human cardiac troponin I HcTnI-K6-H5-D.  
XX Troponin I; immunoassay; assay; analysis; human; cardiac muscle;  
KW skeletal muscle; injury; myocardial infarction; diagnosis; HcTnI-K6-H5-D.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX WO9739132-A1.  
XX  
XX PD 23-OCT-1997;  
XX  
XX PF 14-APR-1997; 97WO-US006147.  
XX  
XX PR 16-APR-1996; 96US-0015772P.  
XX PR 11-APR-1997; 97US-00833743.  
XX  
XX (UYMI-) UNIV MIAMI.  
XX  
XX Potter JD;

XX WPI; 1998-062676/06.  
DR N-PSDB; AAV04221.  
XX  
XX Immunoassay of mammalian troponin using stable standard for comparison -  
PT specifically acid-dialysed solution or its lyophilisate used for  
PT diagnosis of cardiac or skeletal muscle damage.  
XX  
XX Example 2; Page 64-65; 94pp; English.  
XX  
XX This polypeptide comprises a C-terminally modified cardiac troponin I  
CC protein, designated HcTnI-K6-H5-D, comprising human cardiac troponin I  
CC (HcTnI) modified to add 6 lysines, 5 histidines and one aspartate  
CC residue. This modification was made to alter the isoelectric point of the  
CC protein, thereby improving its solubility and stability. A polynucleotide  
CC (see AAV04221) encoding the modified HcTnI was produced by PCR  
CC amplification of a HcTnI cDNA template, and was inserted into vector pBT  
CC lld to allow expression of HcTnI-K6-H5-D in Escherichia coli  
CC transformants. The invention provides an assay for measuring mammalian,  
CC preferably human, troponin in a patient sample. The assay involves  
CC comparing the level in the sample with a novel troponin protein standard.  
CC This is a storage stable, soluble troponin, a functional fragment of the  
CC troponin, a modified troponin or its functional fragment, a troponin  
CC fusion protein or a hetero-multimeric troponin complex (see AAW41570-  
CC 75). The method is used to monitor changes in the level of human  
CC troponin, particularly for diagnosis of diseases involving damage to  
CC heart or skeletal muscle, e.g. acute myocardial infarction. It may also  
CC be used to study normal and pathological functions of troponin-expressing  
CC tissues  
XX  
XX Sequence 222 AA;  
SQ  
Query Match 100.0%; Score 495; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.2e-48;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MADSSDAAREPRPAPAPIRRRSSNYRAYATPEPHAKKSKISASRKLQKLTLLQIAKOE 60  
DB 1 MADSSDAAREPRPAPAPIRRRSSNYRAYATPEPHAKKSKISASRKLQKLTLLQIAKOE 60  
OY 61 LERAEEREGKGRALSTRCOPLELAGLGFAPLQDLCRQ 99  
DB 61 LERAEEREGKGRALSTRCOPLELAGLGFAPLQDLCRQ 99  
RESULT 15  
ABO14731  
ID ABO14731 standard; protein; 222 AA.  
XX  
XX ABO14731;  
XX  
XX 25-AUG-2003 (first entry)  
XX  
XX Novel human protein #104.  
XX  
XX Human; NOV; gene therapy; endocrine related disease; diabetes;  
KW Metabolism-related disease; obesity; central nervous system disorder;  
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;  
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;  
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;  
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;  
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;  
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;  
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;  
KW stroke; infection.  
XX  
XX Homo sapiens.  
OS  
XX WO2003023002-A2.  
XX  
XX PD 20-MAR-2003.  
XX  
XX 09-SEP-2002; 2002WO-US028539.  
XX PF

Search completed: August 30, 2005, 12:05:55  
Job time : 167 secs